## 世界知的所有権機関

## **PCT**

## 国際事務局



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1993年11月12日(12.11.93)

ЛР

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(81) 指定国

AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, JP, KG, KR, KZ, LK, LR, LT, LV, MD, MG, MN, NO, NZ, PL, RO, RU, SI, SK, TJ, TT, UA, US, UZ, VN, 欧州特許(AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI特許(BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG), ARIPO特許(KE, MW, SD, SZ).

添付公開書類

国際調査報告書

補正書

(54) Title: GENE SIGNATURE

(54) 発明の名称 ジーン・シグナチャー

(57) Abstract

A 3'-directed cDNA library which accurately reflects the abundance ratio of mRNA in a cell has been prepared from various human tissues, and sequencing of the cDNAs contained in the library has been conducted to examine the incidence of each cDNA in each tissue. As each cDNA has expression information with each tissue corresponding to the mRNA concentration, these cDNAs are usable as a probe or primer for detecting cell anomaly or discriminating cells. The cloned gene can produce proteins utilizable as a medicine or the like.

WO 95/14772 PCT/JP94/01916

TAATCANTGT TATTGTGTTC CANTITAACT GGGTTAAATG TITN 284

配列番号:3190 配列の長さ:282 配列の型:核酸 トポロジー:直鎖状 クローン名:HUMGS03761

配列:

GATCTCGACT CCCCCTGGC CACAGACCCC CAGGTCATTG TGTTCACTGT ACTCTGTGGG 60
CAAGGATGGG TCCAGAAGAC CCCACTTCAG GCACTAAGAG GGGCTGGACC TNTGCGGCAG 120
GAAGCCAAAG AGACTGGGCC TAGGCCAGGA GTTCCCAAAT NTGAGGGGCG AGAAACAAGA 180
CAAGCTCCTC CCTTGAGAAT TCCCTGTGGA TTTTTAAAAC AGATATTATT TTTNTNATTA 240
TTGTGACAAA ATGTTGNTAA ATGGGATATT AAATAGAATA AA 282

配列番号:3191 配列の長さ:279 配列の型:核酸 トポロジー:直鎖状 クローン名:HUMGS03762

配列:

GATCTGGAGA AGTAAGATGG CCAAATAAAA GCCTCTACCA ATCATCCTCC CCACAGGAAC 60
ACCAAATTTA AGAACTATCT ACACAAAAAA GCACCTTCAT AAGAACCAAA AATCAGAGAG 120
AACAAGGATA AAGAAGTATC CAAATACAAA GAAAATGTTA TGCAAGTGAC CTTTAGAGAT 180
GTTTTAAAGA TGACAAAATA TTGATGANGA TGGGCCAACA AGTGTTACTG TTACCTCTAA 240
TAAAGTTTCA TCACTAGTTT CACCATGGTT AATTGGAAA 279

配列番号:3192 配列の長さ:277 配列の型:核酸 トポロジー:直鎖状 クローン名:HUMGS03763

配列:

配列番号:3193 配列の長さ:277 配列の型:核酸 トポロジー:直鎖状 クローン名:EUMGS03764

配列:

GATCACAGGG AGCCTGTGTT TGTTGGAGGT GTTCCAGAAT CTNTACTGAC ACCACGCTTG 60

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Transor massage.

New Tumor Necrosis Factor family receptor polypeptides and ligands -

By Gevelopmental or gestational abnormalities

Example VII; Fig 13B; 156pp; English.

Example VII; Fig 13B; 156pp; English.

CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active

Creceptor polypeptides: APO4, APO6, APO8 and APO9 or their active

CC receptor polypeptides: APO4 is useful for diagnosing prostate cancer

CC platermining levels of APO4 in an individual. Prostate cancer

CC platermining levels of APO4 in an individual. Prostate cancer

CC platermining levels of APO4 in an individual. Prostate cancer

CC platermining levels of APO4 in an individual. Prostate cancer

CC platermining levels of APO4 in an individual. Prostate cancer

CC platermining levels of APO4 in an individual. Prostate cancer

CC platermining levels of APO4 in an individual. Prostate cancer

CC platermining levels of APO4 in an individual. Prostate cancer

CC plater active polypeptides are also useful for identifying selective

CC platermining levels are also useful for identifying of expressed on the cell surface. The binding is preferably performed in

CC vivo. APO4 polypeptides/ active fragments are also useful for screening

CC agonists and antagonists by binding and observing the changer in APO4

activity. Effective pharmacological agents useful in diagnosis or
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P-PSDB; W93591.
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treatment of disease are also identified using APO4 polypeptides/active fragments and APO4 signal transducer molecules that specifically interact with a cytoplasmic domain of APO4 and detecting a change in level of APO4 activity. The method is performed in vivo or in vitro. APO polypeptides are all useful as immunogens for preparing antibodies. APO4 is also useful for diagnosis/treatment of developmental or gestational abnormalities. APO8 was transfected to human breast carcinoma cell line Sequence 701 BP; 139 A; 210 C; 203 G; 149 T;
                                                                                                                                                                                                                                                                                                                  399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.

WO9514772-A1.
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                                                                                                                                                      Length 701;
                                                                                                                                               Score 519.2; DB 1; Length
Pred. No. 1.8e-99;
0; Mismatches 83; Indels
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Human gene signature HUMGS03761.
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Best Local Similarity 87.3%;
Matches 569; Conservative
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11-NOV-1994; J01916.
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UYEC-) UNIV EAST CAROLINA.

WPI; 99-229400/19.

09-JUN-1998; US-093972.

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A single-stranded DNA (or its complementary strand or the corresp. A single-stranded DNA) which complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences close in T19001-T25687 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from translated sequence is unique to a particular mRNA species, almost untranslated sequence is unique to a particular mRNAs. Each library is constructed so as to reflect accurately the relative abundance of all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 282 BP; 80 A; 62 C; 69 G; 66 T;
                                                                                                                                  Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
12-NOV-1993; JP-355504
                                                                                  Okubo K;
                            (MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
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1171 CAAGGATGGGTCCAGAAGACCCCACTTCAGGCACTAAGAGGGGCTGGACCTG-GCGGCAG 1229 1111 GATCTCGACTCCCCCCTGGCCACAGACCCCCAGGGCATTGTGTTTCACTGTACTCTGTGGG 1170 61 CAAGGATGGGTCCAGAAGACCCCACTTCAGGCACTAAGAGGGGCTGGACCTNTGCGGCAG 120 ij 17.9%; Score 245.4; DB 1; Length 282; Indels ; 9 Pred. No. 1e-42; 0; Mismatches 97.38; Matches 257; Conservative Similarity Query Match Local 1230 ò 윱 à ò g ò a

1350 TIGIGACAAATGTIGATAAATGG 1373 241 TIGIGACAAAIGITGNIAAAIGG 264 셤 ö

X53491 standard; DNA; 114955 BP X53491; RESULT X53491,

pulmonary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiration; asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary disconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis; Human adenosine Al receptor antisense oligonucleotide fragment. Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; 05-JUL-1999 (first entry) prostate cancer; ss. 

25-MAR-1999. 14 SEP-1998; U19419. Synthetic. WO9913886-A1.

Pasconstriction describes antisense oligonuclectides (X52869-X55271)

The specification describes antisense oligonuclectides (X52869-X55271)

The specification describes antisense oligonuclectides genes, dead directed against at least 2 minks selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, dene coding and non-coding and non-coding cregions and all segments of RNAs encoding proteins associated with one cor more diseases, conditions or mixtures. The antisense oligonucleotides (specifically X55180-271) can be used for the antisense cigonucleotides (specifically X55180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded respiration, callergic rhinitis, acute asthma, allergies, asthma, impeded respiration, pulmonary vasoconstriction, emphysema, chronic obstructive preparatory distress syndrome, pain, cystic fibrosis, pulmonary colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastase or have cancer, hepatocellular lungs, including breast and prostate cancer.

Sequence 114955 BP; 6071 A; 29417 C; 35712 G; 21328 T; New antisense oligonucleotides used in treatment of, e.g. pulmonary vasoconstriction 

ö Gaps 5.1%; Score 70.4; DB 1; Length 114955; 32.7%; Pred. No. 6.5e-06; tive 58; Mismatches 316; Indels 0; Best\_Local Similarity 32.7% Matches 182; Conservative Query Match

DD 105272 CCGCCCGCCGCGCGCGCCNNHNNNSCGGCCCGGCCGCGCGCCCCNNHNNNSCGCCCGGC 105213 à

105212 GGGGGGGGGGCGCCCNNHNNNSCGGCCGGGCGGCGGCGCCCVNNHNNNSCGGCCCGGCC 105153 86 AGGCACAGCCCCCCCCCCCATGCCCGCCGTCGGAGCCAGAGGCGGAGGGGGCCCGGG 145 ö

Db 105152 GGGGGGGGCCCCYGNNHNNNSCGGCCCGGCGGCGCGCGCCCCVGGNNHNNNSCGGCCCG 105093 à

Db 105092 GCCGGCGCGCGCCCVGGCNNHNNNSCGGCCGGCGGCGCGCGCCCCVGGCCNHHNNNS 105033 GCCTCGGCCTCCTGCCGGTGGTCAGTTTGGGGAGCCGGGCATCGCTGTCCGCCCAGG 206 ö

266 AGCCTGCCCAGGAGGAGCTGGTGGCAGAGGAGGACCAGGACCGGTCGGAACTGAATCCCC å

DD 104972 CCVGNNHNNNSCGGCCGGCCGGCGGCGCGCCCVGGCCVGCCNHNNNSCGGCCGGCCGG 104913 326 AGACAGAAGAAAGCCAGGATCCTGCGCCTTTCCTGAACCGACTAGTTCGGCCTCGCAGAA 385

Db 104912 CGGCGCGCCCVGGCCVGCGNNHNNNSGCCVGCGGNNHNNNSVGGCCVGCGGNNHNNNSC 104853 445 386 GTGCACCTAAAGGCCGGAAAACACGGGCTCGAAGAGCGATCGCAGCCCATTATGAAGTTC

Db 104852 VGGCCVGCGGNNHNNNSCCVGGCCVGCGGNNHNNNSCCCVGGCCVGCGGGNNHNNNSGCCC 104793

DD 104792 VGGCCVGCGGNHHNNNSCGCCCVGGCCVGCGGNHHNNNSGCGCCCVGGCCVGCGGNHHNN 104733 506 AGGAAGCCAGAATCAACAGCTCCAGCCCTCTGCGCTACAACCGCCAGATCGGGGAGTTTA 565

566 TAGTCACCCGGGCTGG 581 ð